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## Amendments to Claims

Claim 1. (Currently Amended) A An isolated carotenoid overproducing E. colibacteria-comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway wherein the dxs, idi and ygbBP genes are overexpressed and wherein the yjeR gene is down regulated and wherein the dxs, idi and ygbBP and yjeR genes are derived from either E. coli or Methylomonas.

Claim 2. (Currently Amended) A An isolated carotenoid overproducing bacteria E. coli comprising the genes encoding a functional carotenoid enzymatic biosynthetic pathway wherein the dxs, idi, ygbBP and ispB genes are overexpressed, and wherein the dxs, idi, ygbBP and ispB genes are derived either from E. coli or Methylomonas.

Claim 3. (Currently Amended) The carotenoid overproducing basteria-E. coli of Claim 1 or 2 wherein the lytB and dxr gene is optionally overexpressed and wherein the lytB and dxr genes are derived from E. coli or Methylomonas.

ispB lytB and dxr yjeR

Claim 4. (Currently Amended) The carotenoid overproducing bacteria E. coli of Claim 1 or 2 wherein the carotenoid enzymatic biosynthetic pathway consists of the genes dxs, dxr, ygpP, ychB, ygbB, lytB, idi, ispA, ispB crtE, crtB, crtI, and crtY.

Claim 5. (Currently Amended) The carotenoid overproducing bacteria-E. coli of Claim 4 wherein the carotenoid enzymatic biosynthetic pathway optionally additionally comprises the crtZ and crtW genes.

Claim 6-8. (Canceled)

Claim 9. (Currently amended) The carotenoid overproducing bacteria-E. coli of any of Claims 1 - 3 of Claims 1 or 2 wherein the dxs, idi, ispB and ygbBP genes are under the control of a strong promoter.

Claim 10. (Currently Amended) The carotenoid overproducing bacteria- $\underline{E}$ . coli of Claim 9 wherein the strong promoter is selected from the group consisting of lac, ara, tet, trp,  $\lambda P_L$ ,  $\lambda P_R$ , T7, tac,  $P_{T5}$ , and trc.

Claim 11. (Currently amended) The carotenoid overproducing bacteria E. coli of any of Claims 1 3 either of Claims 1 or 2 wherein the dxs, idi, ispB and ygbBP genes are integrated in multicopy in the bacterial chromosome.

Claim 12. (Currently amended) The carotenoid overproducing bacteria E. coli of any of Claims 1-3 either of Claims 1 or 2 wherein the dxs, idi, ispB and ygbBP genes are present in multicopy in the bacteria on one or more plasmids.

Claim 13. (Currently Amended) The carotenoid overproducing bacteria of of Claim 17 wherein the *yjeR* gene is down regulated by gene disruption.

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Claim 14. (Currently Amended) The carotenoid overproducing bacteria-E. coli of Claim 13 wherein the disrupted *yjeR* gene has the nucleotide sequence as set forth in SEQ ID NO:63.

Claim 15. (Currently amended) The carotenoid overproducing bacteria-E. coli of either of any of Claims 1—3—Claims 1 or 2 wherein the dxs, idi, ispB ygbBP and lytB genes are chromosomally integrated into the host cell genome.

Claim 16. (Currently Amended) A carotenoid overproducing bacteria E. coli selected from the group consisting of: a strain having the ATCC identification number PTA-4807 and a strain having the ATCC identification number PTA-4823.

Claim 17. (Withdrawn) A method for the production of a carotenoid comprising:

- a) growing the carotenoid overproducing bacteria of any of Claims 1-5, the bacteria overexpressing at least one gene selected from the group consisting of dxs, idi ygbBP, ispB, lytB, dxr, wherein yjeR is optionally downregulated, for a time sufficient to produce a carotenoid; and
- b) optionally recovering the carotenoid from the carotenoid overproducing bacteria of step (a).

Claim 18. (Withdrawn) A method according to Claim 17 wherein the carotenoid is selected from the group consisting of antheraxanthin, adonixanthin, astaxanthin, canthaxanthin, capsorubrin,  $\beta$ -cryptoxanthin, didehydrolycopene, didehydrolycopene,  $\beta$ -carotene,  $\zeta$ -carotene,  $\gamma$ -carotene,  $\gamma$ -carotene,

keto- $\gamma$ -carotene,  $\psi$ -carotene,  $\epsilon$ -carotene,  $\beta$ , $\psi$ -carotene, torulene, echinenone, gamma-carotene, zeta-carotene, alpha-cryptoxanthin, diatoxanthin, 7,8-didehydroastaxanthin, fucoxanthin, fucoxanthinol, isorenieratene,  $\beta$ -isorenieratene lactucaxanthin, lutein, lycopene, neoxanthin, neurosporene, hydroxyneurosporene, peridinin, phytoene, rhodopin, rhodopin glucoside, siphonaxanthin, spheroidene, spheroidenone, spirilloxanthin, uriolide, uriolide acetate, violaxanthin, zeaxanthin- $\beta$ -diglucoside, zeaxanthin, and C30-carotenoids.

Claim 19. (Withdrawn) A method according to Claim 18 wherein the carotenoid is produced at a level of at least about 6 mg per gram dry cell weight.

Claim 20. (Withdrawn) A method according to Claim 18 wherein the bacteria is selected from the group consisting Agrobacterium, Erythrobacter, Chlorobium, Chromatium, Flavobacterium, Cytophaga, Rhodobacter, Rhodococcus, Streptomyces, Brevibacterium, Corynebacteria, Mycobacterium, Deinococcus, Paracoccus, Escherichia, Bacillus, Myxococcus, Salmonella, Yersinia, Erwinia, Pantoea, Pseudomonas, Sphingomonas, Methylomonas, Methylobacter, Methylococcus, Methylosinus, Methylomicrobium, Methylocystis, Alcaligenes, Synechocystis, Synechococcus, Anabaena, Thiobacillus, Methanobacterium, Klebsiella, and Myxococcus.

Claim 21. (Withdrawn) A method according to Claim 20 wherein the bacteria is E. coli.

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Claim 22. (Withdrawn) A method according to Claim 17 wherein the dxs, idi, ygbBP, ispB and lytB genes are under the control of a promoter selected from the group consisting of lac, ara, tet, trp,  $\lambda P_L$ ,  $\lambda P_R$ , T7, tac,  $P_{T5}$ , and trc.

Claim 23. (Withdrawn) A method according to Claim 17 wherein the dxs, idi, ispB, ygbBP and lytB genes are integrated in multicopy in the bacterial chromosome.

Claim 24. (Withdrawn) A method according to Claim 17 wherein the dxs, idi, ispB, ygbBP and lytB genes are in multicopy in the bacteria on one or more plasmids.

Claim 25. (Withdrawn) A method according to Claim 17 wherein the *yjeR* gene is down regulated by gene disruption.

Claim 26. (Withdrawn) A method according to Claim 25 wherein the disrupted yieR gene has the nucleotide sequence as set forth in SEQ ID NO:63.

Claim 27. (Withdrawn) A method according to Claim 17 wherein the dxs, idi ispB, ygbBP and lytB genes are chromosomally integrated into the host cell genome.